



## SEQUENCE LISTING

<110> Hosted, Jr., Thomas J.  
Horan, Ann C.

<120> Isolation of *Micromonospora carbonacea* var *africana*  
pMLP1 integrase and use of integrating function for  
site-specific integration into *Micromonospora*  
*halophilica* and *Micromonospora carbonacea* chromosome

<130> IN01164K

<140> 09/855,340  
<141> 2001-05-15

<150> 60/204,670  
<151> 2000-05-17

<160> 16

<170> PatentIn Ver. 2.1

<210> 1  
<211> 1179  
<212> DNA  
<213> *Micromonospora carbonacea*

<400> 1  
gtgtggatcg agaagaacgg gcccgtctac cgcattcggg acctcggtcg cggtaaaaag 60  
gtcaccattc agaccggta tccgacgaag accagcgcca agaatgcgtat ggtgcagttc 120  
cgtgcggagc agttgcaggg caacgcgctc atgcccgcgcg gcggtcagat taccctcgcc 180  
gatttcgtgg gggagtggtt gccgagctac gaaaagacgc tgaaaccgac cgccgtgaac 240  
tcggagggca accggatccg caaccacctc ctgcccatac tcggccatct cacccttgac 300  
gagctggacg ggcaggtcac ccagcagtgg gtcaacgacc tggaggccgg cgtcgccccc 360  
tggccggagt ccacgcgggg tctgtcggaaag ccgctggcag cgaagacgtat cagcaactgc 420  
cacggcctgc tgacacacgtat ctgcggcgcg gcgatcgccg cgaaacggat caggctcaac 480  
ccgtgctctt cgacgtatgtt gccccggcgc gagccgaaag agatgaagtt cctgagcgac 540  
ccggagatcg gtcggcttat cacggcgtt ccggccact ggcgaccgct cgtcatgctg 600  
ctggcggcga ccggctctgag gtgggtgag gcgatcgccc tgccgcggg ccgggtcgac 660  
ctgctcgccg cgccggcccg gctgaccgtc gtcgagcgc tccaggagct gcccagcacc 720  
ggagagctcg tcttccagtc gccaagagacc gccaaggggcc ggcgacccgt cagtttacc 780  
acgaaagtcg ctctactgt tacgccactc atcgcggaa agaaaagtga cgaggtcgt 840  
ttcacccgcgca gaaaaaggccg gatggtaagg acgcgcattat tccggccgat ctgggtcaag 900  
gcgtgcgagg aagccggctt tccgggctta cgcattcaccg atctgcggca cactcacgcg 960  
gcgcattcgtat tttctggccgg gctgtccgtt tcggcgatct cccgcggcct cggtcactcg 1020  
tcgcattcgtt tcacggatct gctgtacggg cacctgcgtt aggaggtcga cgaggggatc 1080  
ctcgccgcga tcgaggagcc gatggccggc gtccgggctg aggaccttggaa ggcggaaactc 1140  
gacgaggagc tgacggacgt gttggccgac gcagcatga 1179

<210> 2  
<211> 426  
<212> DNA  
<213> *Micromonospora carbonacea*

<400> 2  
atgcgcacaaca caccggggct ggggcgcggc acatgggccc catacgtcct caccggccgc 60  
gagcgcggccg gactgacccaa gagcggatgg gccaggcgca tccagaagga cggggccacc 120  
gtcgccgggt gggaggacgg caagaaccgg cccgacgcgc cggacccgt tggccgcgtc 180  
gcccagggtgc tcggcctcga cctcgacgaa gcccgcgcg cccgacccgt ggcggccggc 240  
gtcaccggccgc cagcgcacccaa aaccatggac ctggacgagg aaatcgagct ggtccgcacc 300

gaccccaagc tggacgagga catgaagcgg cgcatcatcg ccctaattcct ggagcgccgt 360  
 gagcgcgaca aggccgcggc gatcgaggaa accaagcggc tcatcgacct gttccgcccgg 420  
 agctga 426

<210> 3  
 <211> 34  
 <212> DNA  
 <213> *Micromonospora carbonacea*

<400> 3  
 ccccggtacg ggttcaattc ccatcagtca cccg 34

<210> 4  
 <211> 241  
 <212> DNA  
 <213> *Micromonospora carbonacea*

<400> 4  
 tattagtccg cacgcccggc ggcccccggc gaggcgagcg catggggct gtagctcagt 60  
 tggcagagca ccgggttggc gtccgggttgc tcgtgggttc aattcccatc agtcacccgt 120  
 acacgaaggc cccctccact cggagggggc ctccggcgtt cctgagggtt cgccgtcagg 180  
 cggtcggctc ggcgctgggg gactcgcccc cgtcggcggg agtggctcg gcgtccgggg 240  
 a 241

<210> 5  
 <211> 243  
 <212> DNA  
 <213> *Micromonospora carbonacea*

<400> 5  
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 tggggctgt agtcagtttgc gcaagggcacc ggggttggcgtt cccgggttgcgttgggttcaa 120  
 ttcccatcag tcacccggca agtggatcta ctccacagca gatcaggccc cctccgaaga 180  
 gggggcctga tgcgtcatag gggacaggtt gggaaactca accccggct cttgtctcg 240  
 gtc 243

<210> 6  
 <211> 247  
 <212> DNA  
 <213> *Micromonospora carbonacea*

<400> 6  
 tagggaaatc cactccggag acgccccggag caatccggag catgacggag caaccagcag 60  
 gtcaggtggc ctgttgcacc cctgaccagg gccccgggtac gggttcaatt cccatcagtc 120  
 acccgtagac gaaggcccccc tccactcgga gggggcccttc ggcgttcctg agggttcgcg 180  
 gtcaggcggtt cggctcgccg ctggggactt cggccggctc ggcgggagtg gcctcggcgt 240  
 ccgggg 247

<210> 7  
 <211> 255  
 <212> DNA  
 <213> *Micromonospora halophytica*

<400> 7  
 ttctccgca cccgccccggg gcgttcgacc ggggtcgccggc gcatgggtggc ttttagctcag 60  
 ttggcagagc accgggttgcgtt ggtccgggtt caattcccat cagtcacccc 120

aggtaagacc caggtcaggg ccgttctca cggccctga cgcatttca gggcatggt 180  
 ggggcgcta cgggggtgg ggtgtctac cgcgagccag catctcgatc aggcgatcga 240  
 gccggcgctg ccggg 255

<210> 8  
 <211> 315  
 <212> DNA  
 <213> *Micromonospora halophytica*

<400> 8  
 tttcccgca cccgcccggg gcgttcgacc gggtgccggc gcatggtggc ttagctcag 60  
 ttggcagagc accgggttgt ggtcccggtt gtcgtgggtt caattccat cagtcacccg 120  
 gcaagtggat ctactccaca gcagatcagg cccctccga agagggggcc tgcgtcgtca 180  
 taggggacag gttaggggaaac tcaacccccc gtccttgcgt cgcgtccgggt catgccgtcc 240  
 gcgtacccct ccgcgtaccc ggcctctcc cgttcctcga tctcggccggc gagctgatcg 300  
 cgcaggtgcg cctcc 315

<210> 9  
 <211> 260  
 <212> DNA  
 <213> *Micromonospora halophytica*

<400> 9  
 taggggaatc cactccggag acgcccggag caatccggag catgacggag caaccagcag 60  
 gtcaggtggc ctgttgaccc cctgaccagg gccccggtac gggttcaatt cccatcagtc 120  
 accccaggtt agaccaggat cagggccggt ttcaccggc cctgacgcatt ttcaggggc 180  
 atgggggggg cgctaccggg ggtgggtgt ctcaccgcga gccagcatct cgatcaggcg 240  
 atcgagccgg cgctgcccggg 260

<210> 10  
 <211> 209  
 <212> DNA  
 <213> artificial sequence

<220>

<223> pMLP1 attP region

<400> 10  
 taggggaatc cactccggag acgcccggag caatccggag catgacggag caaccagcag 60  
 gtcaggtggc ctgttgaccc cctgaccagg gccccggtac gggttcaatt cccatcagtc 120  
 accccggcaag tggatctact ccacagcaga tcaggcccc tccgaagagg gggctgatg 180  
 cgtcataggg gacaggtagg ggaactcaa 209

<210> 11  
 <211> 19

<212> DNA

<213> artificial sequence

<220>

<223> primer PR144

<400> 11

tgcttcgacg ccatcargg

19

<210> 12

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> primer PR145

<220>

<221> misc\_feature

<222> (7)..(7)

<223> n is inosine (I)

<400> 12

gtggaanccg ccgaakccgc

20

<210> 13

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> primer PDH504

<400> 13

aggcaacaa gggaaagcgta

20

<210> 14

<211> 21

<212> DNA

<213> artificial sequence

<220>

<223> primer PDH505

<400> 14

ggcgggggtg tggctattat t

21

<210> 15

<211> 21

<212> PRT

<213> artificial sequence

<220>

<223> amino acid sequence of open reading frame indicated in figures 4b and 4d

<400> 15

Ser Pro Asp Ala Glu Ala Thr Pro Ala Asp Gly Ala Glu Ser Pro Ser  
1 5 10 15

Ala Glu Pro Thr Ala  
20

<210> 16

<211> 21

<212> PRT

<213> artificial sequence

<220>

<223> amino acid sequence of open reading frame indicated in figures 5b and 5d

<400> 16

Arg Gln Arg Arg Leu Asp Arg Leu Ile Glu Met Leu Ala Arg Gly Glu  
1 5 10 15

Thr Pro His Pro Arg  
20